

SEQUENCE LISTING

<110> Bradfield, Christopher A.
 Dolwick, Kristin M.
 Carver, Lucy A.

<120> Ah Receptor cDNAs and Genetically Engineered Cells for
 Detecting Agonists to the Ah Receptor

<130> HYBRIDZYME

<140>

<141>

<160> 40

<170> PatentIn Ver. 2.1

<210> 1

<211> 3207

<212> DNA

<213> murine

<220>

<221> CDS

<222> (1)..(2415)

<400> 1

atg agc agc ggc gcc aac atc acc tat gcc agc cgc aag cgg cgc aag	48
Met Ser Ser Gly Ala Asn Ile Thr Tyr Ala Ser Arg Lys Arg Arg Lys	
1 5 10 15	
ccg gtg cag aaa aca gta aag ccc atc ccc gct gaa gga att aag tca	96
Pro Val Gln Lys Thr Val Lys Pro Ile Pro Ala Glu Gly Ile Lys Ser	
20 25 30	
aat cct tct aag cga cac aga gac cgg ctg aac aca gag tta gac cgc	144
Asn Pro Ser Lys Arg His Arg Asp Arg Leu Asn Thr Glu Leu Asp Arg	
35 40 45	
ctg gcc agc ctg ctg ccc ttc ccg caa gat gtt att aat aag ctg gac	192
Leu Ala Ser Leu Leu Pro Phe Pro Gln Asp Val Ile Asn Lys Leu Asp	
50 55 60	
aaa ctc tct gtt ctt agg ctc agc gtc acg tac ctg agg gcc aag agc	240
Lys Leu Ser Val Leu Arg Leu Ser Val Thr Tyr Leu Arg Ala Lys Ser	
65 70 75 80	
ttc ttt gat gtt gca tta aag tcc acc cct gct gac aga aat gga ggc	288
Phe Phe Asp Val Ala Leu Lys Ser Thr Pro Ala Asp Arg Asn Gly Gly	
85 90 95	
cag gac cag tgt aga gca caa atc aga gac tgg cag gat ttg caa gaa	336
Gln Asp Gln Cys Arg Ala Gln Ile Arg Asp Trp Gln Asp Leu Gln Glu	
100 105 110	
gga gag ttc ttg tta cag gcg ctg aat ggc ttt gtg ctg gtt gtc aca	384
Gly Glu Phe Leu Leu Gln Ala Leu Asn Gly Phe Val Leu Val Val Thr	

115	120	125	
gca gat gcc ttg gtc ttc tat gct tcc tcc act atc caa gat tac ctg Ala Asp Ala Leu Val Phe Tyr Ala Ser Ser Thr Ile Gln Asp Tyr Leu 130 135 140			432
ggc ttt cag cag tct gat gtc atc cat cag agc gta tat gag ctc atc Gly Phe Gln Gln Ser Asp Val Ile His Gln Ser Val Tyr Glu Leu Ile 145 150 155 160			480
cat aca gaa gac cgg gcg gaa ttc cag cgc cag ctt cac tgg gct cta His Thr Glu Asp Arg Ala Glu Phe Gln Arg Gln Leu His Trp Ala Leu 165 170 175			528
aac cca gac tct gca caa gga gtg gac gaa gcc cat ggc cct cca cag Asn Pro Asp Ser Ala Gln Gly Val Asp Glu Ala His Gly Pro Pro Gln 180 185 190			576
gca gca gtc tat tat acc cca gac cag ctt cct cca gag aac gct tct Ala Ala Val Tyr Tyr Thr Pro Asp Gln Leu Pro Pro Glu Asn Ala Ser 195 200 205			624
ttc atg gag agg tgc ttc agg tgc cgg ctg agg tgc ctg ctg gat aat Phe Met Glu Arg Cys Phe Arg Cys Arg Leu Arg Cys Leu Leu Asp Asn 210 215 220			672
tca tct ggt ttt ctg gca atg aat ttc caa ggg agg tta aag tat ctt Ser Ser Gly Phe Leu Ala Met Asn Phe Gln Gly Arg Leu Lys Tyr Leu 225 230 235 240			720
cat gga cag aac aag aaa ggg aag gac gga gcg ctg ctt cct cca caa His Gly Gln Asn Lys Lys Gly Lys Asp Gly Ala Leu Leu Pro Pro Gln 245 250 255			768
ctg gct ttg ttt gca ata gct act cca ctt cag cca ccc tcc atc ctg Leu Ala Leu Phe Ala Ile Ala Thr Pro Leu Gln Pro Pro Ser Ile Leu 260 265 270			816
gaa att cga acc aaa aac ttc atc ttc agg acc aaa cac aag cta gac Glu Ile Arg Thr Lys Asn Phe Ile Phe Arg Thr Lys His Lys Leu Asp 275 280 285			864
ttc aca cct att ggt tgt gat gcc aaa ggg cag ctt att ctg ggc tat Phe Thr Pro Ile Gly Cys Asp Ala Lys Gly Gln Leu Ile Leu Gly Tyr 290 295 300			912
aca gaa gta gag ctg tgc aca aga gga tgc ggg tac cag ttc atc cat Thr Glu Val Glu Leu Cys Thr Arg Gly Ser Gly Tyr Gln Phe Ile His 305 310 315 320			960
gct gca gac ata ctt cac tgt gca gaa tcc cac atc cgc atg att aag Ala Ala Asp Ile Leu His Cys Ala Glu Ser His Ile Arg Met Ile Lys 325 330 335			1008
act gga gaa agt ggc atg aca gtt ttc cgg ctt ctt gca aaa cac agt Thr Gly Glu Ser Gly Met Thr Val Phe Arg Leu Leu Ala Lys His Ser 340 345 350			1056

cgc tgg agg tgg gtc cag tcc aat gca cgc ttg att tac aga aat gga Arg Trp Arg Trp Val Gln Ser Asn Ala Arg Leu Ile Tyr Arg Asn Gly 355 360 365	1104
aga cca gat tac atc atc gcc act cag aga cca ctg acg gat gaa gaa Arg Pro Asp Tyr Ile Ile Ala Thr Gln Arg Pro Leu Thr Asp Glu Glu 370 375 380	1152
gga cga gag cat tta cag aag cga agt acg tcg ctg ccc ttc atg ttt Gly Arg Glu His Leu Gln Lys Arg Ser Thr Ser Leu Pro Phe Met Phe 385 390 395 400	1200
gct acc gga gag gct gtg ttg tac gag atc tcc agc cct ttc tct ccc Ala Thr Gly Glu Ala Val Leu Tyr Glu Ile Ser Ser Pro Phe Ser Pro 405 410 415	1248
ata atg gat ccc cta cca ata cgc acc aaa agc aac act agc agg aaa Ile Met Asp Pro Leu Pro Ile Arg Thr Lys Ser Asn Thr Ser Arg Lys 420 425 430	1296
gac tgg gct ccc cag tca acc cca agt aag gat tct ttc cac ccc agt Asp Trp Ala Pro Gln Ser Thr Pro Ser Lys Asp Ser Phe His Pro Ser 435 440 445	1344
tct ctt atg agt gcc ctc atc cag cag gat gag tcc atc tat ctg tgt Ser Leu Met Ser Ala Leu Ile Gln Gln Asp Glu Ser Ile Tyr Leu Cys 450 455 460	1392
cct cct tca agc cct gcg ctg tta gac agc cat ttt ctc atg ggc tcc Pro Pro Ser Ser Pro Ala Leu Leu Asp Ser His Phe Leu Met Gly Ser 465 470 475 480	1440
gtg agc aag tgc ggg agt tgg caa gac agc ttt gcg gcc gca gga agt Val Ser Lys Cys Gly Ser Trp Gln Asp Ser Phe Ala Ala Ala Gly Ser 485 490 495	1488
gag gct gcg ctg aaa cat gag caa att ggc cat gct cag gac gtg aac Glu Ala Ala Leu Lys His Glu Gln Ile Gly His Ala Gln Asp Val Asn 500 505 510	1536
ctt gca ctc tct ggc ggc ccc tca gag ctc ttt ccg gat aat aaa aat Leu Ala Leu Ser Gly Gly Pro Ser Glu Leu Phe Pro Asp Asn Lys Asn 515 520 525	1584
aat gac ttg tac agc atc atg agg aac ctt ggg att gat ttt gaa gat Asn Asp Leu Tyr Ser Ile Met Arg Asn Leu Gly Ile Asp Phe Glu Asp 530 535 540	1632
atc aga agc atg cag aac gag gag ttc ttc aga act gac tcc acc gct Ile Arg Ser Met Gln Asn Glu Glu Phe Phe Arg Thr Asp Ser Thr Ala 545 550 555 560	1680
gct ggt gag gtt gac ttc aaa gac atc gac ata acg gac gaa atc ctg Ala Gly Glu Val Asp Phe Lys Asp Ile Asp Ile Thr Asp Glu Ile Leu 565 570 575	1728
acc tac gtg cag gat tcc ctg aac aat tca act ttg ctg aac tcg gct Thr Tyr Val Gln Asp Ser Leu Asn Asn Ser Thr Leu Leu Asn Ser Ala	1776

580	585	590	
tgc cag cag cag cct gtg act cag cac cta agc tgt atg ctg cag gag Cys Gln Gln Gln Pro Val Thr Gln His Leu Ser Cys Met Leu Gln Glu 595 600 605			1824
cgc ctg caa cta gag caa cag caa cag ctt cag cag ccc ccg ccg cag Arg Leu Gln Leu Glu Gln Gln Gln Gln Leu Gln Gln Pro Pro Pro Gln 610 615 620			1872
gct ctg gag ccc cag cag cag ctg tgt cag atg gtg tgc ccc cag caa Ala Leu Glu Pro Gln Gln Gln Leu Cys Gln Met Val Cys Pro Gln Gln 625 630 635 640			1920
gat ctg ggt ccg aag cac acg caa atc aac ggc acg ttt gca agt tgg Asp Leu Gly Pro Lys His Thr Gln Ile Asn Gly Thr Phe Ala Ser Trp 645 650 655			1968
aac ccc acc cct ccc gtg tct ttc aac tgt ccc cag cag gaa cta aag Asn Pro Thr Pro Pro Val Ser Phe Asn Cys Pro Gln Gln Glu Leu Lys 660 665 670			2016
cac tat cag ctc ttt tcc agc tta cag ggg act gct cag gaa ttt ccc His Tyr Gln Leu Phe Ser Ser Leu Gln Gly Thr Ala Gln Glu Phe Pro 675 680 685			2064
tac aaa cca gag gtg gac agt gtg cct tac aca cag aac ttt gct ccc Tyr Lys Pro Glu Val Asp Ser Val Pro Tyr Thr Gln Asn Phe Ala Pro 690 695 700			2112
tgt aat cag cct ctg ctt cca gaa cat tcc aag agt gtg cag ttg gac Cys Asn Gln Pro Leu Leu Pro Glu His Ser Lys Ser Val Gln Leu Asp 705 710 715 720			2160
ttc cct gga agg gat ttt gaa ccg tcc ctg cat ccc act act tct aat Phe Pro Gly Arg Asp Phe Glu Pro Ser Leu His Pro Thr Thr Ser Asn 725 730 735			2208
tta gat ttt gtc agt tgt tta caa gtt cct gaa aac caa agt cat ggg Leu Asp Phe Val Ser Cys Leu Gln Val Pro Glu Asn Gln Ser His Gly 740 745 750			2256
ata aac tca cag tcc gcc atg gtc agt cct cag gca tac tat gct ggg Ile Asn Ser Gln Ser Ala Met Val Ser Pro Gln Ala Tyr Tyr Ala Gly 755 760 765			2304
gcc atg tcc atg tat cag tgc cag cca ggg cca cag cgc acc cct gtg Ala Met Ser Met Tyr Gln Cys Gln Pro Gly Pro Gln Arg Thr Pro Val 770 775 780			2352
gac cag acg cag tac agc tct gaa att cca ggt tct cag gca ttc cta Asp Gln Thr Gln Tyr Ser Ser Glu Ile Pro Gly Ser Gln Ala Phe Leu 785 790 795 800			2400
agc aag gtg cag agt tgaggtgttt tcaatgaaac ctattcgtcc gacttgagca Ser Lys Val Gln Ser 805			2455

gcattggcca cgctgctcag accactggcc atctccatca ctgcggaagc ccggcctctt 2515
 cccgatatca cacccggtgg attcctgtag ctcccatgcc aggatgaaat tcattcagga 2575
 acaggatacc agaactgtga gggttggaca tcagtacact ttctccaaaa cagatttcga 2635
 ttcttgtgtt tagagaagga gtttaaaacc cgtacctgag atgctcccta tacgatggga 2695
 gagctcggac ggagcacatg ggaggagttc aggcacctca gagtgcacag tgtttactgt 2755
 gaaaaattct cgggttccct gctcagtaac ttcagcagga aaaacaggga ggtatttgga 2815
 gctttgaact tctggattct tgtagtata ccaaatacgg agttacagga ctaaccgatt 2875
 tcctatatatt tttaacctct gttttgtcc cagaagttaa agtaaatggt ttggtgcttt 2935
 tctcaaaaga aaatctcaat gctttctttc tgcactgtta atataagtgc ctactttttt 2995
 gttgttggtg ttgttggttt ctgatttttt tctttttttc tatctacctg taacacaata 3055
 gggtatgtat tttatatgaa atatttttta tcttttttga attaataattc tttctgcaca 3115
 aagaaagttt cccgaatccc aacctttcta tgaccocgct gtgtgtgtgc actactcatc 3175
 ctttccttca gataaagagt aattgataac tc 3207

<210> 2
 <211> 805
 <212> PRT
 <213> murine

<400> 2
 Met Ser Ser Gly Ala Asn Ile Thr Tyr Ala Ser Arg Lys Arg Arg Lys
 1 5 10 15
 Pro Val Gln Lys Thr Val Lys Pro Ile Pro Ala Glu Gly Ile Lys Ser
 20 25 30
 Asn Pro Ser Lys Arg His Arg Asp Arg Leu Asn Thr Glu Leu Asp Arg
 35 40 45
 Leu Ala Ser Leu Leu Pro Phe Pro Gln Asp Val Ile Asn Lys Leu Asp
 50 55 60
 Lys Leu Ser Val Leu Arg Leu Ser Val Thr Tyr Leu Arg Ala Lys Ser
 65 70 80
 Phe Phe Asp Val Ala Leu Lys Asn Gly Gly
 85 95
 Gln Asp Gln Cys Arg Ala Gln Leu Gln Glu
 100 110
 Gly Glu Phe Leu Leu Gln Ala Val Val Thr
 115
 Ala Asp Ala Leu Val Phe Tyr Ala Ser Ser Thr Ile Gln Asp Tyr Leu

130					135					140					
Gly	Phe	Gln	Gln	Ser	Asp	Val	Ile	His	Gln	Ser	Val	Tyr	Glu	Leu	Ile
145					150					155					160
His	Thr	Glu	Asp	Arg	Ala	Glu	Phe	Gln	Arg	Gln	Leu	His	Trp	Ala	Leu
				165					170					175	
Asn	Pro	Asp	Ser	Ala	Gln	Gly	Val	Asp	Glu	Ala	His	Gly	Pro	Pro	Gln
			180					185					190		
Ala	Ala	Val	Tyr	Tyr	Thr	Pro	Asp	Gln	Leu	Pro	Pro	Glu	Asn	Ala	Ser
		195					200					205			
Phe	Met	Glu	Arg	Cys	Phe	Arg	Cys	Arg	Leu	Arg	Cys	Leu	Leu	Asp	Asn
	210					215					220				
Ser	Ser	Gly	Phe	Leu	Ala	Met	Asn	Phe	Gln	Gly	Arg	Leu	Lys	Tyr	Leu
225					230					235					240
His	Gly	Gln	Asn	Lys	Lys	Gly	Lys	Asp	Gly	Ala	Leu	Leu	Pro	Pro	Gln
				245					250					255	
Leu	Ala	Leu	Phe	Ala	Ile	Ala	Thr	Pro	Leu	Gln	Pro	Pro	Ser	Ile	Leu
			260					265					270		
Glu	Ile	Arg	Thr	Lys	Asn	Phe	Ile	Phe	Arg	Thr	Lys	His	Lys	Leu	Asp
		275					280					285			
Phe	Thr	Pro	Ile	Gly	Cys	Asp	Ala	Lys	Gly	Gln	Leu	Ile	Leu	Gly	Tyr
	290					295					300				
Thr	Glu	Val	Glu	Leu	Cys	Thr	Arg	Gly	Ser	Gly	Tyr	Gln	Phe	Ile	His
305					310					315					320
Ala	Ala	Asp	Ile	Leu	His	Cys	Ala	Glu	Ser	His	Ile	Arg	Met	Ile	Lys
				325					330					335	
Thr	Gly	Glu	Ser	Gly	Met	Thr	Val	Phe	Arg	Leu	Leu	Ala	Lys	His	Ser
			340					345					350		
Arg	Trp	Arg	Trp	Val	Gln	Ser	Asn	Ala	Arg	Leu	Ile	Tyr	Arg	Asn	Gly
		355					360					365			
Arg	Pro	Asp	Tyr	Ile	Ile	Ala	Thr	Gln	Arg	Pro	Leu	Thr	Asp	Glu	Glu
	370				375						380				
Gly	Arg	Glu	His	Leu	Gln	Lys	Arg	Ser	Thr	Ser	Leu	Pro	Phe	Met	Phe
385					390					395					400
Ala	Thr	Gly	Glu	Ala	Val	Leu	Tyr	Glu	Ile	Ser	Ser	Pro	Phe	Ser	Pro
				405					410					415	
Ile	Met	Asp	Pro	Leu	Pro	Ile	Arg	Thr	Lys	Ser	Asn	Thr	Ser	Arg	Lys
			420				425					430			
Asp	Trp	Ala	Pro	Gln	Ser	Thr	Pro	Ser	Lys	Asp	Ser	Phe	His	Pro	Ser
		435					440					445			

Ser Leu Met Ser Ala Leu Ile Gln Gln Asp Glu Ser Ile Tyr Leu Cys
 450 455 460
 Pro Pro Ser Ser Pro Ala Leu Leu Asp Ser His Phe Leu Met Gly Ser
 465 470 475 480
 Val Ser Lys Cys Gly Ser Trp Gln Asp Ser Phe Ala Ala Ala Gly Ser
 485 490 495
 Glu Ala Ala Leu Lys His Glu Gln Ile Gly His Ala Gln Asp Val Asn
 500 505 510
 Leu Ala Leu Ser Gly Gly Pro Ser Glu Leu Phe Pro Asp Asn Lys Asn
 515 520 525
 Asn Asp Leu Tyr Ser Ile Met Arg Asn Leu Gly Ile Asp Phe Glu Asp
 530 535 540
 Ile Arg Ser Met Gln Asn Glu Glu Phe Phe Arg Thr Asp Ser Thr Ala
 545 550 555 560
 Ala Gly Glu Val Asp Phe Lys Asp Ile Asp Ile Thr Asp Glu Ile Leu
 565 570 575
 Thr Tyr Val Gln Asp Ser Leu Asn Asn Ser Thr Leu Leu Asn Ser Ala
 580 585 590
 Cys Gln Gln Gln Pro Val Thr Gln His Leu Ser Cys Met Leu Gln Glu
 595 600 605
 Arg Leu Gln Leu Glu Gln Gln Gln Gln Leu Gln Gln Pro Pro Pro Gln
 610 615 620
 Ala Leu Glu Pro Gln Gln Gln Leu Cys Gln Met Val Cys Pro Gln Gln
 625 630 635 640
 Asp Leu Gly Pro Lys His Thr Gln Ile Asn Gly Thr Phe Ala Ser Trp
 645 650 655
 Asn Pro Thr Pro Pro Val Ser Phe Asn Cys Pro Gln Gln Glu Leu Lys
 660 665 670
 His Tyr Gln Leu Phe Ser Ser Leu Gln Gly Thr Ala Gln Glu Phe Pro
 675 680 685
 Tyr Lys Pro Glu Val Asp Ser Val Pro Tyr Thr Gln Asn Phe Ala Pro
 690 695 700
 Cys Asn Gln Pro Leu Leu Pro Glu His Ser Lys Ser Val Gln Leu Asp
 705 710 715 720
 Phe Pro Gly Arg Asp Phe Glu Pro Ser Leu His Pro Thr Thr Ser Asn
 725 730 735
 Leu Asp Phe Val Ser Cys Leu Gln Val Pro Glu Asn Gln Ser His Gly
 740 745 750
 Ile Asn Ser Gln Ser Ala Met Val Ser Pro Gln Ala Tyr Tyr Ala Gly

<210>	3
<211>	5261
<212>	DNA
<213>	human

<400> 3																
aattccgcac	ggcccagacc	caggattctt	tatagacggc	ccaggctcct	cctccgcccg	60										
ggccgcctca	cctgcgggca	ttgcgcgccg	cctccgcgcg	tgtagacggc	acctgcgcgcg	120										
ccttgctcgc	gggtctccgc	cctcgcccac	cctcactgcg	ccaggcccag	gcagctcacc	180										
tgtactggcg	cgggctgcgg	aagctgcgtg	acgcgaggcg	ttgaggcgcg	gcgcccacgc	240										
cactgtcccc	agaggacgca	ggtggagcgg	gcgcgacttc	gcgaaccgcg	cgccggccgc	300										
cgcagtggtc	ccagcctaca	ccgggttccg	gggaccgcgc	cgccagtgcc	cggggagtag	360										
ccgcccgcgt	cggctgggca	cc	atg	aac	agc	agc	agc	gcc	aac	atc	acc	tac	412			
			Met	Asn	Ser	Ser	Ser	Ala	Asn	Ile	Thr	Tyr	10			
			1					5								
gcc	agt	cgc	aag	cgg	cgg	aag	ccg	gtg	cag	aaa	aca	gta	aag	cca	atc	460
Ala	Ser	Arg	Lys	Arg	Arg	Lys	Pro	Val	Gln	Lys	Thr	Val	Lys	Pro	Ile	
			15						20					25		
cca	gct	gaa	gga	atc	aag	tca	aat	cct	tcc	aag	cgg	cat	aga	gac	cga	508
Pro	Ala	Glu	Gly	Ile	Lys	Ser	Asn	Pro	Ser	Lys	Arg	His	Arg	Asp	Arg	
			30					35					40			
ctt	aat	aca	gag	ttg	gac	cgt	ttg	gct	agc	ctg	ctg	cct	ttc	cca	caa	556
Leu	Asn	Thr	Glu	Leu	Asp	Arg	Leu	Ala	Ser	Leu	Leu	Pro	Phe	Pro	Gln	
			45				50					55				
gat	gtt	att	aat	aag	ttg	gac	aaa	ctt	tca	gtt	ctt	agg	ctc	agc	gtc	604
Asp	Val	Ile	Asn	Lys	Leu	Asp	Lys	Leu	Ser	Val	Leu	Arg	Leu	Ser	Val	
	60					65					70					
agt	tac	ctg	aga	gcc	aag	agc	ttc	ttt	gat	gtt	gca	tta	aaa	tcc	tcc	652
Ser	Tyr	Leu	Arg	Ala	Lys	Ser	Phe	Phe	Asp	Val	Ala	Leu	Lys	Ser	Ser	
	75				80					85					90	

cac atg cag aat gaa aaa ttt ttc aga aat gat ttt tct ggt gag gtt His Met Gln Asn Glu Lys Phe Phe Arg Asn Asp Phe Ser Gly Glu Val 555 560 565 570	2092
gac ttc aga gac att gac tta acg gat gaa atc ctg acg tat gtc caa Asp Phe Arg Asp Ile Asp Leu Thr Asp Glu Ile Leu Thr Tyr Val Gln 575 580 585	2140
gat tct tta agt aag tct ccc ttc ata cct tca gat tat caa cag caa Asp Ser Leu Ser Lys Ser Pro Phe Ile Pro Ser Asp Tyr Gln Gln Gln 590 595 600	2188
cag tcc ttg gct ctg aac tca agc tgt atg gta cag gaa cac cta cat Gln Ser Leu Ala Leu Asn Ser Ser Cys Met Val Gln Glu His Leu His 605 610 615	2236
cta gaa cag caa cag caa cat cac caa aag caa gta gta gtg gag cca Leu Glu Gln Gln Gln Gln His His Gln Lys Gln Val Val Val Glu Pro 620 625 630	2284
cag caa cag ctg tgt cag aag atg aag cac atg caa gtt aat ggc atg Gln Gln Gln Leu Cys Gln Lys Met Lys His Met Gln Val Asn Gly Met 635 640 645 650	2332
ttt gaa aat tgg aac tct aac caa atc gtg cct ttc aat tgt cca cag Phe Glu Asn Trp Asn Ser Asn Gln Ile Val Pro Phe Asn Cys Pro Gln 655 660 665	2380
caa gac cca caa caa tat aat gtc ttt aca gac tta cat ggg atc agt Gln Asp Pro Gln Gln Tyr Asn Val Phe Thr Asp Leu His Gly Ile Ser 670 675 680	2428
caa gag ttc ccc tac aaa tct gaa atg gat tct atg cct tat aca cag Gln Glu Phe Pro Tyr Lys Ser Glu Met Asp Ser Met Pro Tyr Thr Gln 685 690 695	2476
aac ttt att tcc tgt aat cag cct gta tta cca caa cat tcc aaa tgt Asn Phe Ile Ser Cys Asn Gln Pro Val Leu Pro Gln His Ser Lys Cys 700 705 710	2524
aca gag ctg gac tac cct atg ggg agt ttt gaa cca tcc cca tac ccc Thr Glu Leu Asp Tyr Pro Met Gly Ser Phe Glu Pro Ser Pro Tyr Pro 715 720 725 730	2572
act act tct agt tta gaa gat ttt gtc act tgt tta caa ctt cct gaa Thr Thr Ser Ser Leu Glu Asp Phe Val Thr Cys Leu Gln Leu Pro Glu 735 740 745	2620
aac caa aag cat gga tta aat cca cag tca gcc ata ata act cct cag Asn Gln Lys His Gly Leu Asn Pro Gln Ser Ala Ile Ile Thr Pro Gln 750 755 760	2668
aca tgt tat gct ggg gcc gtg tcg atg tat cag tgc cag cca gaa cct Thr Cys Tyr Ala Gly Ala Val Ser Met Tyr Gln Cys Gln Pro Glu Pro 765 770 775	2716
cag cac acc cac gtg ggt cag atg cag tac aat cca gta ctg cca ggc Gln His Thr His Val Gly Gln Met Gln Tyr Asn Pro Val Leu Pro Gly	2764

780	785	790	
caa cag gca ttt tta aac aag ttt cag aat gga gtt tta aat gaa aca			2812
Gln Gln Ala Phe Leu Asn Lys Phe Gln Asn Gly Val Leu Asn Glu Thr			
795	800	805	810
tat cca gct gaa tta aat aac ata aat aac act cag act acc aca cat			2860
Tyr Pro Ala Glu Leu Asn Asn Ile Asn Asn Thr Gln Thr Thr Thr His			
	815	820	825
ctt cag cca ctt cat cat ccg tca gaa gcc aga cct ttt cct gat ttg			2908
Leu Gln Pro Leu His His Pro Ser Glu Ala Arg Pro Phe Pro Asp Leu			
	830	835	840
aca tcc agt gga ttc ctg taa ttccaagccc aattttgacc ctggtttttg			2959
Thr Ser Ser Gly Phe Leu			
	845		
gattaaatta gtttgtgaag gattatggaa aaataaaaact gtcactgttg gacgtcagca 3019			
agttcacatg gaggcattga tgcattgctat tcacaattat tccaaaccaa attttaattt 3079			
ttgcttttag aaaaggaggt ttaaaaatgg tatcaaaatt acatatacta cagtcaagat 3139			
agaaaggggtg ctgccacgga gtgggtgaggt accgtctaca tttcacatta ttctggggcac 3199			
cacaaaatat acaaaaacttt atcagggaaa ctaagattct tttaaattag aaaatattct 3259			
ctatttgaat tatttctgtc acagtaaaaa taaaataactt tgagttttga gctactggat 3319			
tcttattagt tcccaaata caaagttaga gaactaaact agtttttct atcatgttaa 3379			
cctctgcttt tatctcagat gttaaaataa atgggttggt gctttttata aaaagataat 3439			
ctcagtgcctt tctctcttca ctgtttcatc taagtgcctc acattttttt ctacctataa 3499			
cactctagga tgtatatattt atataaagta ttctttttct tttttaaatt aatatctttc 3559			
tgcacacaaa tattatttgt gtttcctaaa tccaaccaat tttcattaat tcaggcatat 3619			
tttaactcca ctgcttacct actttcttca ggtaaaaggg caaataatga tcgaaaaaat 3679			
aattatttat tacataattt agttgtttct agactataaa tgttgctatg tgccttatgt 3739			
tgaaaaaatt taaaagtaaa atgtctttcc aaattatttc ttaattatta taaaaatatt 3799			
aagacaatag cacttaaatt cctcaacagt gttttcagaa gaaataaata taccactctt 3859			
tacctttatt gatattctca tgatgatagt tgaatgttgc aatgtgaaaa atctgctgtt 3919			
aactgcaacc ttgtttatta aattgcaaga agctttattt ctagcttttt aattaagcaa 3979			
agcaccatt tcaatgtgta taaattgtct ttaaaaactg ttttagacct ataatccttg 4039			
ataatatatt gtgttgactt tataaatttc gcttcttaga acagtggaaa ctatgtgttt 4099			
ttctcatatt tgaggagtgt taagattgca gatagcaagg tttggtgcaa agtattgtaa 4159			

```

tgagtgaatt gaatggtgca ttgtatagat ataatgaaca aaattatttg taagatatatt 4219
gcagtttttc attttaaaaa gtccatacct tatatatgca ctttaatttgt tggggcttta 4279
catactttat caatgtgtct ttctaagaaa tcaagtaatg aatccaactg cttaaagttg 4339
gtattaataa aaagacaacc acatagttcg tttaccttca aacttttaggt ttttttaatg 4399
atatactgat cttcattacc aataggcaaa ttaatcacco taccaacttt actgtcctaa 4459
catggacttt caaaaagaaa aaatgacacc atcttttatt cttttttttt tttttttttt 4519
gagagagagt cttactctgc cgcccaaact ggagtgcagt ggcacaatct tggctcactg 4579
caacctctac ctctggggtt caagtgatcc tcttgacctca gcctcccgag ttgctgggat 4639
tgcgggcatg gtggcgtgag cctgtagtcc tagctactcg ggaggctgag gcaggagaat 4699
agcctgaacc tgggaatcgg aggttgccagg gccaaagatcg cccactgca ctccagcctg 4759
gcaatagacc gagctccgtc tccaaaaaaa aaaatacaat ttttatttct tttacttttt 4819
ttagtaagtt aatgtatata aaaatggctt cggacaaaat atctctgagt tctgtgtatt 4879
ttcagtcaaa actttaaaacc tgtagaatca atttaagtgt tgaaaaaaat ttgtctgaaa 4939
catttcataa tttgtttcca gcatgaggta tctaaggatt tagaccagag gtctagatta 4999
atactctatt ttacattta aaccttttat tataagtctt acataaacca tttttgttac 5059
tctcttccac atgttactgg ataaattgtt tagtggaata taggcttttt aatcatgaat 5119
atgatgacaa tcagttatac agttataaaa ttaaagttt gaaaagcaat attgtatatt 5179
tttatctata taaaataact aaaatgtatc taagaataat aaaatcacgt taaacccaaa 5239
aaaaaaaaa aaaaaaaaaa aa 5261

```

```

<210> 4
<211> 848
<212> PRT
<213> human

```

```

<400> 4
Met Asn Ser Ser Ser Ala Asn Ile Thr Tyr Ala Ser Arg Lys Arg Arg
 1          5          10          15
Lys Pro Val Gln Lys Thr Val Lys Pro Ile Pro Ala Glu Gly Ile Lys
          20          25          30
Ser Asn Pro Ser Lys Arg His Arg Asp Arg Leu Asn Thr Glu Leu Asp
          35          40          45
Arg Leu Ala Ser Leu Leu Pro Phe Pro Gln Asp Val Ile Asn Lys Leu
          50          55          60
Asp Lys Leu Ser Val Leu Arg Leu Ser Val Ser Tyr Leu Arg Ala Lys
          65          70          75          80
Ser Phe Phe Asp Val Ala Leu Lys Ser Ser Pro Thr Glu Arg Asn Gly
          85          90          95
Gly Gln Asp Asn Cys Arg Ala Ala Asn Phe Arg Glu Gly Leu Asn Leu

```


<220>
 <221> modified_base
 <222> (16)
 <223> i

<220>
 <221> modified_base
 <222> (19)
 <223> i

<220>
 <221> modified_base
 <222> (22)
 <223> i

<220>
 <221> modified_base
 <222> (29)
 <223> i

<220>
 <221> modified_base
 <222> (32)
 <223> i

<220>
 <221> modified_base
 <222> (43)
 <223> i

<220>
 <221> modified_base
 <222> (46)
 <223> i

<400> 5
 ttatnctc tcngcnggna tnggtcttna cngttctttc tgnacnggtc tt

52

<210> 6
 <211> 20
 <212> DNA
 <213> murine

<220>
 <221> modified_base
 <222> (7)
 <223> Can be either adenine, thymine, guanosine or cytosine.

<220>
 <221> modified_base
 <222> (10)
 <223> Can be either adenine, thymine, guanosine or cytosine.

<400> 6
 aaagccngtn caagaaagac

20

<210> 7
 <211> 25
 <212> DNA
 <213> murine

<400> 7
 ggatttgact taattccttc agggg 25

<210> 8
 <211> 40
 <212> DNA
 <213> human

<400> 8
 ccatcgatct cgagagattg cagatagcaa ggtttggtgc 40

<210> 9
 <211> 38
 <212> DNA
 <213> human

<400> 9
 ccatcgatct cgagtgaat gagtgaattg aatggtgc 38

<210> 10
 <211> 30
 <212> DNA
 <213> human

<400> 10
 gaagatcttc cagtgggtccc agcctacacc 30

<210> 11
 <211> 30
 <212> DNA
 <213> human

<400> 11
 gaagatcttc atgtgaactt gctgacgtcc 30

<210> 12
 <211> 63
 <212> DNA
 <213> murine

<400> 12
 gctctagatg atcaccatgg tgcagaagac cgtgaagccc atccccgctg aaggaattaa 60
 gtc 63

<210> 13
 <211> 63

<212> DNA
<213> murine

<400> 13
gcactagttg atcaccatgg ccagccgcaa gcggcgcaag ccggtgcaga agaccgtgaa 60
gcc 63

<210> 14
<211> 65
<212> DNA
<213> murine

<400> 14
gcactagttg atcaccatga gcagcggcgc caacatcacc tatgccagcc gcaagcgccg 60
caagc 65

<210> 15
<211> 20
<212> DNA
<213> murine

<400> 15
gcagagtctg ggttttagagc 20

<210> 16
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
sequence

<400> 16
tcgagtagat cacgcaatgg gcccgagc 27

<210> 17
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
sequence

<400> 17
tcgagctggg cccattgcgt gatctac 27

<210> 18
<211> 28
<212> DNA
<213> Unknown Organism

<220>

<223> Description of Unknown Organism: unknown

<400> 18

gcgtcgactg ggcacccatga acagcagc

28

<210> 19

<211> 40

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Unknown

<400> 19

cccaagctta cgcgtgggttc tctggaggaa gctggtctgg

40

<210> 20

<211> 36

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Unknown

<400> 20

cccaagctta cgcgtggaag tctagcttgt gtttgg

36

<210> 21

<211> 36

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Unknown

<400> 21

cccaagctta cgcgtgaagc cggaaaactg tcatgc

36

<210> 22

<211> 49

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Unknown

<400> 22

cccaagctta cgcgtgcagt ggtctctgag tggcgatgat gtaatctgg

49

<210> 23

<211> 37

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Unknown

<400> 23

cccaagctta cgcgtggtct ttgaagtcaa cctcacc

37

<210> 24

<211> 26

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Unknown

<400> 24

gaattgtaat acgactcact ataggg

26

<210> 25

<211> 20

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Unknown

<400> 25

cgctcgagaa ctagtgatc

20

<210> 26

<211> 21

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Unknown

<400> 26

agctgcttaa ttaattaagc a

21

<210> 27

<211> 21

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Unknown

<400> 27

agcttgctta attaattaag c

21

<210> 28

<211> 34
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Unknown

<400> 28
 gcgtcgactg atgagcagcg gcgccaacat cacc 34

<210> 29
 <211> 20
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Unknown

<400> 29
 cattacttat ctagagctcg 20

<210> 30
 <211> 19
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Unknown

<400> 30
 gatttaggtg acactatag 19

<210> 31
 <211> 49
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Unknown

<400> 31
 gataagaatg cggccgcacg gatccagcag caacagcaaa cagaattgg 49

<210> 32
 <211> 38
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Unknown

<400> 32
 ataagaatgc ggccgcagcc ccccgaccg atgtcagc 38

<210> 33
 <211> 37
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Unknown

<400> 33
 atagtttagc ggccgccccca ccgtactcgt caattcc 37

<210> 34
 <211> 37
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Unknown

<400> 34
 gccgtcgacg cgcccgcgaa gtctagcttg tgtttgg 37

<210> 35
 <211> 36
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Unknown

<400> 35
 ataagaatgc ggccgcaccc tcaatgttgt gtcggg 36

<210> 36
 <211> 40
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Unknown

<400> 36
 cgggatcctc gcggccgcag agaatttcag gaatagtggc 40

<210> 37
 <211> 72
 <212> PRT
 <213> human

<400> 37
 Arg Lys Arg Arg Lys Pro Val Gln Lys Thr Val Lys Pro Ile Pro Ala
 1 5 10 15

Glu Gly Ile Lys Ser Asn Pro Ser Lys Arg His Arg Asp Arg Leu Asn

20 25 30
 Thr Glu Leu Asp Arg Leu Ala Ser Leu Leu Pro Phe Pro Gln Asp Val
 35 40 45
 Ile Asn Lys Leu Asp Lys Leu Ser Val Leu Arg Leu Ser Val Ser Tyr
 50 55 60
 Leu Arg Ala Lys Ser Phe Phe Asp
 65 70

<210> 38
 <211> 72
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: unknown

<400> 38
 Arg Lys Arg Arg Lys Pro Val Gln Lys Thr Val Lys Pro Ile Pro Ala
 1 5 10 15
 Glu Gly Ile Lys Ser Asn Pro Ser Lys Arg His Arg Asp Arg Leu Asn
 20 25 30
 Thr Glu Leu Asp Arg Leu Ala Ser Leu Leu Pro Phe Pro Gln Asp Val
 35 40 45
 Ile Asn Lys Leu Asp Lys Leu Ser Val Leu Arg Leu Ser Val Thr Tyr
 50 55 60
 Leu Arg Ala Lys Ser Phe Phe Asp
 65 70

<210> 39
 <211> 208
 <212> PRT
 <213> human

<400> 39
 Glu Phe Gln Arg Gln Leu His Trp Ala Leu Asn Pro Ser Gln Cys Thr
 1 5 10 15
 Glu Ser Gly Gln Gly Ile Glu Glu Ala Thr Gly Leu Pro Gln Thr Val
 20 25 30
 Val Cys Tyr Asn Pro Asp Gln Ile Pro Pro Glu Asn Ser Pro Leu Met
 35 40 45
 Glu Arg Cys Phe Ile Cys Arg Leu Arg Cys Leu Leu Asp Asn Ser Ser
 50 55 60
 Gly Phe Leu Ala Met Asn Phe Gln Gly Lys Leu Lys Tyr Leu His Gly
 65 70 75 80

Gln Lys Lys Lys Gly Lys Asp Gly Ser Ile Leu Pro Pro Gln Leu Ala
 85 90 95
 Leu Phe Ala Ile Ala Thr Pro Leu Gln Pro Pro Ser Ile Leu Glu Ile
 100 105 110
 Arg Thr Lys Asn Phe Ile Phe Arg Thr Lys His Lys Leu Asp Phe Thr
 115 120 125
 Pro Ile Gly Cys Asp Ala Lys Gly Arg Ile Val Leu Gly Tyr Thr Glu
 130 135 140
 Ala Glu Leu Cys Thr Arg Gly Ser Gly Tyr Gln Phe Ile His Ala Ala
 145 150 155 160
 Asp Met Leu Tyr Cys Ala Glu Ser His Ile Arg Met Ile Lys Thr Gly
 165 170 175
 Glu Ser Gly Met Ile Val Phe Arg Leu Leu Thr Lys Asn Asn Arg Trp
 180 185 190
 Thr Trp Val Gln Ser Asn Ala Arg Leu Leu Tyr Lys Asn Gly Arg Pro
 195 200 205

<210> 40
 <211> 204
 <212> PRT
 <213> murine

<400> 40
 Glu Phe Gln Arg Gln Leu His Trp Ala Leu Asn Pro Asp Ser Ala Gln
 1 5 10 15
 Gly Val Asp Glu Ala His Gly Pro Pro Gln Ala Ala Val Tyr Tyr Thr
 20 25 30
 Pro Asp Gln Leu Pro Pro Glu Asn Ala Ser Phe Met Glu Arg Cys Phe
 35 40 45
 Arg Cys Arg Leu Arg Cys Leu Leu Asp Asn Ser Ser Gly Phe Leu Ala
 50 55 60
 Met Asn Phe Gln Gly Arg Leu Lys Tyr Leu His Gly Gln Asn Lys Lys
 65 70 75 80
 Gly Lys Asp Gly Ala Leu Leu Pro Pro Gln Leu Ala Leu Phe Ala Ile
 85 90 95
 Ala Thr Pro Leu Gln Pro Pro Ser Ile Leu Glu Ile Arg Thr Lys Asn
 100 105 110
 Phe Ile Phe Arg Thr Lys His Lys Leu Asp Phe Thr Pro Ile Gly Cys
 115 120 125

Asp	Ala	Lys	Gly	Gln	Leu	Ile	Leu	Gly	Tyr	Thr	Glu	Val	Glu	Leu	Cys
130						135					140				
Thr	Arg	Gly	Ser	Gly	Tyr	Gln	Phe	Ile	His	Ala	Ala	Asp	Ile	Leu	His
145					150					155					160
Cys	Ala	Glu	Ser	His	Ile	Arg	Met	Ile	Lys	Thr	Gly	Glu	Ser	Gly	Met
				165					170					175	
Thr	Val	Phe	Arg	Leu	Leu	Ala	Lys	His	Ser	Arg	Trp	Arg	Trp	Val	Gln
			180					185					190		
Ser	Asn	Ala	Arg	Leu	Ile	Tyr	Arg	Asn	Gly	Arg	Pro				
	195						200								